

# SEQUENCE LISTING

<110> DeVico et al, Anthony

<120> VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE

<130> 4115-144 CIP

<160> 33

<170> PatentIn version 3.1

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<211> 2159

<212> DNA

<213> Artificial Sequence

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<223> Synthesized construct

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Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val  
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln  
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr  
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Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly  
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Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala  
325 330 335

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340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro  
355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys  
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Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser  
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Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro  
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Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu  
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Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala  
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Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys  
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Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr  
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Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser  
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Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly  
580 585 590

Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr  
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Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val  
610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser  
625 630 635 640

Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln  
645 650 655

Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser  
660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val  
675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu  
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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu  
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val  
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Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val  
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met  
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Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
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Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser  
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn  
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe  
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr  
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys  
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe  
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys

TO THE 0307660





Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys  
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Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala  
485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly  
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Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys  
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Lys Val Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr  
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Ala Ser Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln  
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Ile Lys Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser  
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Lys Leu Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly  
580 585 590

Asn Phe Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr  
595 600 605

Tyr Ile Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val  
610 615 620

Phe Gly Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser  
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Leu Thr Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln  
645 650 655

Cys Arg Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser  
660 665 670

Val Ser Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val  
675 680 685

Leu Gln Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu  
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Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr  
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Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu
35          40          45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val
50          55          60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val
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Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met
85          90          95

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Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser  
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn  
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe  
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr  
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys  
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe  
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys  
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val  
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val  
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln  
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr  
290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly  
305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala  
325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln  
340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro  
355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys  
370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser  
385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys  
405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro  
420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu  
435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg  
450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys  
465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala  
485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Thr Gly Ser Ser Gly Gly Gly  
500 505 510

Gly Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Cys  
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Asn Leu Ala Arg Cys Gln Leu Arg Cys Lys Ser Leu Gly Leu Leu Gly  
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Lys Cys Ala Gly Ser Phe Cys Ala Cys Gly Pro Xaa

Protein = 0904060

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550

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195

200

205

Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser  
210 215 220

Arg Ala Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg  
225 230 235 240

Glu Gln Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly  
245 250 255

Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe  
260 265 270

Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu  
275 280 285

Glu Ser Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg  
290 295 300

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr  
305 310 315 320

Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly  
325 330 335

Leu Leu Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val  
340 345 350

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu  
355 360 365

Tyr Lys Tyr Lys Val Val Lys Ile Gly Ser Ser Gly Gly Gly Gly Ser  
370 375 380

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ala Ala Lys Lys Val  
385 390 395 400

Val Leu Gly Lys Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser  
405 410 415

Gln Lys Lys Ser Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys  
420 425 430

Ile Leu Gly Asn Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu  
 435 440 445

Asn Asp Arg Ala Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe  
 450 455 460

Pro Leu Ile Ile Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile  
 465 470 475 480

Cys Glu Val Glu Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly  
 485 490 495

Leu Thr Ala Asn Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr  
 500 505 510

Leu Thr Leu Glu Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg  
 515 520 525

Ser Pro Arg Gly Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser  
 530 535 540

Gln Leu Glu Leu Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln  
 545 550 555 560

Asn Gln Lys Lys Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Glu  
 565 570 575

Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr  
 580 585 590

<210> 14  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthesized construct

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(15)  
 <223> X can be any amino acid

<400> 14

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Xaa Tyr Val Xaa Thr  
 1 5 10 15

<210> 15  
 <211> 111  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized construct

<400> 15  
 ggggggtacca tgcccatggg gtctctgcaa ccgctggcca ccttgtagct gctgggggatg 60  
 ctgggtcgctt cctgcctcgg aaagaacgtg accgagaact tcaacatgtg g 111

<210> 16  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized construct

<400> 16  
 ggggggatccg atcttcacca ccttgatctt gtacagctc 39

<210> 17  
 <211> 75  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized construct

<400> 17  
 ctgtgcgtga ccctggggcgc ggccgagatg aagaactgca gcttcaacat cggcgcgggc 60  
 cgctgatca gctgc 75

<210> 18  
 <211> 75  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized construct

<400> 18  
 gcagctgatc aggcggcccg cgccgatgtt gaagctgcag ttcttcatct cgcccgcgcc 60  
 cagggtcacg cacag 75

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[illegible]

gaattcttag gggccgcagg cgcagaagct gccggcgcac ttgccagca ggcccaggct 60  
 cttgcagcgc agctggcagc gggccagggt gcaagcggcc gc 102

<210> 23  
 <211> 1518  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized construct

<400> 23  
 atgcccatgg ggtctctgca accgctggcc accttgacc tgctggggat gctggtcgct 60  
 tctgcctcg gaaacgccga ggagaagctg tgggtgaccg tgtactacgg cgtgcccgctg 120  
 tggaaggagg ccaccaccac cctgttctgc gccagcgacc gcaaggccta cgacaccgag 180  
 gtgcacaacg tgtggggccac ccacgcctgc gtgcccaccg accccaaccc ccaggagggtg 240  
 gagctgaaga acgtgaccga gaacttcaac atgtggaaga acaacatggt ggagcagatg 300  
 cacgaggaca tcatcagcct gtgggaccag agcctgaagc cctgcgtgaa gctgaccccc 360  
 ctgtgcgtga ccctgaactg caccgacctg cgcaacgcc ccaacggcaa cgacaccaac 420  
 accactagta gcagccgcgg catggtgggc ggcggcgaga tgaagaactg cagcttcaac 480  
 atcaccacca acatccgcgg caaggtgcag aaggagtacg ccctgttcta caagctggac 540  
 atcgccccca tcgacaacaa cagcaacaac cgctaccgcc tgatcagctg caacaccagc 600  
 gtgatcacc aggcctgccc caaggtgagc ttcgagccca tccccatcca ctactgcgcc 660  
 cccgccggct tcgccatcct gaagtgaag gacaagaagt tcaacggcaa gggcccctgc 720  
 accaacgtga gcaccgtgca gtgcacccac ggcattccgc ccgtggtgag caccagctg 780  
 ctgctgaacg gcagcctggc cgaggaggag gtggtgatcc gcagcgccaa cttcgccgac 840  
 aacgccaagg tgatcatcgt gcagctgaac gagagcgtgg agatcaactg caccgcccc 900  
 aacaacaaca cccgcaagtc catccacatc ggccccggcc gcgccttcta caccaccggc 960  
 gagatcatcg gcgacatccg ccaggccac tgcaacctga gccgcgcaa gtggaacgac 1020  
 accctgaaca agatcgtgat caagctgcgc gagcagttcg gcaacaagac catcgtgttc 1080  
 aagcacagca gcggcggcga ccccgagatc gtgaccaca gcttcaattg cggcggcgag 1140  
 ttctttctact gcaacagcac ccagctgttc aacagcacct ggaacgtgac cgaggagagc 1200  
 aacaacaccg tggagaacaa caccatcacc ctgccctgcc gcatcaagca gatcatcaac 1260  
 atgtggcagg aggtgggccc cgccatgtac gccccccca tccgcggcca gatccgctgc 1320

agttchaaca tcaccggcct gctgctgacc cgcgacggcg gccccgagga caacaagacc 1380  
gaggtgttcc gccccggcgg cggcgacatg cgcgacaact ggcgcagcga gctgtacaag 1440  
tacaaggtgg tgaagatcga gcccctgggc gtggcccca ccaaggccaa gcgccgcgtg 1500  
gtgcagcgcg agaagcgt 1518

<210> 24  
<211> 506  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> Synthesized construct  
<400> 24

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly  
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val  
20 25 30

Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu  
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val  
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val  
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met  
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser  
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn

00024050-00000000



160

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr  
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys  
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe  
210 215 220

Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly Pro Cys  
225 230 235 240

Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val  
245 250 255

Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val  
260 265 270

Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile Val Gln  
275 280 285

Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr  
290 295 300

Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Gly  
305 310 315 320

Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala  
325 330 335

Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg Glu Gln  
340 345 350

Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly Asp Pro  
355 360 365

Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys  
370 375 380

Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu Glu Ser  
385 390 395 400

Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg Ile Lys  
405 410 415

Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr Ala Pro  
420 425 430

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu  
435 440 445

Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val Phe Arg  
450 455 460

Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys  
465 470 475 480

Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala  
485 490 495

Lys Arg Arg Val Val Gln Arg Glu Lys Arg  
500 505

<210> 25  
<211> 534  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthesized construct

<400> 25  
aagaaagtgg tgctgggcaa aaaaggggat acagtggaac tgacctgtac agcttcccag 60  
aagaagagca tacaattcca ctggaaaaac tccaaccaga taaagattct gggaaatcag 120  
ggctccttct taactaaagg tccatccaag ctgaatgac gcgctgactc aagaagaagc 180  
ctttgggacc aaggaaactt cccctgac atcaagaatc ttaagataga agactcagat 240  
acttacatct gtgaagtgga ggaccagaag gaggaggtgc aattgctagt gttcggattg 300  
actgccaact ctgacacca cctgcttcag gggcagagcc tgaccctgac cttggagagc 360  
ccccctggta gtagccctc agtgcaatgt aggagtccaa ggggtaaaaa catacagggg 420




Leu Ala

<210> 27  
<211> 1128  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthesized construct

<400> 27  
atgcccatgg ggtctctgca accgctggcc accttgtacc tgctggggat gctgggtcgct 60  
tcttgccctcg gaaagaacgt gaccgagaac ttcaacatgt ggaagaacaa catgggtggag 120  
cagatgcacg aggacatcat cagcctgtgg gaccagagcc tgaagccctg cgtgaagctg 180  
acccccctgt gcgtgaccct gggcgcgggc gagatgaaga actgcagctt caacatcggc 240  
gcggggccgcc tgatcagctg caacaccagc gtgatcacc aggccctgcc caaggtgagc 300  
ttcgagccca tccccatcca ctactgcgc cccgcccggct tcgccatcct gaagtgaag 360  
gacaagaagt tcaacggcaa gggcccctgc accaacgtga gcaccgtgca gtgcaccac 420  
ggcatccgcc ccgtggtgag caccagctg ctgctgaacg gcagcctggc cgaggaggag 480  
gtggtgatcc gcagcgccaa cttcgccgac aacgccaaagg tgatcatcgt gcagctgaac 540  
gagagcgtgg agatcaactg caccgcgcc aacaacaaca cccgaagtc catccacatc 600  
ggccccggcc gcgccttcta caccaccggc gagatcatcg gcgacatccg ccaggccac 660  
tgcaacctga gccgcgcaa gtggaacgac accctgaaca agatcgtgat caagctgcgc 720  
gagcagttcg gcaacaagac catcgtgttc aagcacagca gcggcggcga ccccgagatc 780  
gtgaccaca gcttcaattg cggcggcgag ttcttctact gcaacagcac ccagctgttc 840  
aacagcacct ggaacgtgac cgaggagagc aacaacaccg tggagaacaa caccatcacc 900  
ctgccctgcc gcatcaagca gatcatcaac atgtggcagg aggtgggccc cgccatgtac 960  
gccccccca tccgcggcca gatccgctgc agttchaaca tcaccggcct gctgctgacc 1020  
cgcgacggcg gccccgagga caacaagacc gaggtgttcc gccccggcgg cggcgacatg 1080  
cgcgacaact ggcgcagcga gctgtacaag tacaaggtgg tgaagatc 1128

<210> 28  
<211> 376  
<212> PRT






<223> Synthesized construct

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly  
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Lys Asn Val Thr Glu Asn Phe Asn  
20 25 30

Met Trp Lys Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser  
35 40 45

Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys  
50 55 60

Val Thr Leu Gly Ala Gly Glu Met Lys Asn Cys Ser Phe Asn Ile Gly  
65 70 75 80

Ala Gly Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys  
85 90 95

Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala  
100 105 110

Gly Phe Ala Ile Leu Lys Cys Lys Asp Lys Lys Phe Asn Gly Lys Gly  
115 120 125

Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro  
130 135 140

Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu
145					150					155					160

Val Val Ile Arg Ser Ala Asn Phe Ala Asp Asn Ala Lys Val Ile Ile  
165 170 175

Val Gln Leu Asn Glu Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn  
180 185 190

Asn Thr Arg Lys Ser Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr  
195 200 205

Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser  
210 215 220

Arg Ala Lys Trp Asn Asp Thr Leu Asn Lys Ile Val Ile Lys Leu Arg  
225 230 235 240

Glu Gln Phe Gly Asn Lys Thr Ile Val Phe Lys His Ser Ser Gly Gly  
245 250 255

Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe  
260 265 270

Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Asn Val Thr Glu  
275 280 285

Glu Ser Asn Asn Thr Val Glu Asn Asn Thr Ile Thr Leu Pro Cys Arg  
290 295 300

Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Arg Ala Met Tyr  
305 310 315 320

Ala Pro Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly  
325 330 335

Leu Leu Leu Thr Arg Asp Gly Gly Pro Glu Asp Asn Lys Thr Glu Val  
340 345 350

Phe Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu  
355 360 365

Tyr Lys Tyr Lys Val Val Lys Ile  
370 375

<210> 29  
<211> 1518  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthesized construct

<400> 29  
atgcccatgg ggtctctgca accgctggcc acctgtacc tgctggggat gctgggtcgct 60



















Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly  
1 5 10 15

Met Leu Val Ala Ser Cys Leu Gly Asn Ala Glu Glu Lys Leu Trp Val  
20 25 30

Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr Thr Leu  
35 40 45

Phe Cys Ala Ser Asp Arg Lys Ala Tyr Asp Thr Glu Val His Asn Val  
50 55 60

Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Val  
65 70 75 80

Glu Leu Lys Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asn Met  
85 90 95

Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu  
100 105 110

Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asn Cys Thr  
115 120 125

Asp Leu Arg Asn Ala Thr Asn Gly Asn Asp Thr Asn Thr Thr Ser Ser  
130 135 140

Ser Arg Gly Met Val Gly Gly Gly Glu Met Lys Asn Cys Ser Phe Asn  
145 150 155 160

Ile Thr Thr Asn Ile Arg Gly Lys Val Gln Lys Glu Tyr Ala Leu Phe  
165 170 175

Tyr Lys Leu Asp Ile Ala Pro Ile Asp Asn Asn Ser Asn Asn Arg Tyr  
180 185 190

Arg Leu Ile Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys  
195 200 205

Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe



220

Pro Ile Arg Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu  
435 440 445

[illegible]



<213> Artificial Sequence

<220>

<223> Synthesized construct

<220>

<221> MISC\_FEATURE

<222> (1)..(259)

<223> X is any amino acid

<400> 32

Met Pro Met Gly Ser Leu Gln Pro Leu Ala Thr Leu Tyr Leu Leu Gly  
1 5 10 15

Met Leu Val Ala Ser Val Leu Ala Asp Pro Glu Glu Pro Lys Ser Cys  
20 25 30

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
35 40 45

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
50 55 60

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
65 70 75 80

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
85 90 95

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
100 105 110

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
115 120 125

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
130 135 140

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
145 150 155 160

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
165 170 175

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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 180 185 190

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 195 200 205

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 210 215 220

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 225 230 235 240

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 245 250 255

Pro Gly Xaa

<210> 33  
 <211> 63  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthesized construct

<400> 33  
 ggatcctctg gtggcggtgg ctcgggctcc ggaggaggtg ggtcgggtgg cggcgcggcc 60  
 gct 63

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